REMARKS

In view of the foregoing claim amendment, and the arguments that follow, applicants submit that all the pending claims are in condition for allowance.

Rejection of Claim 69 Under 35 U.S.C. § 101

The Examiner argues that Claim 69 is not drawn to computer programs and computer memory, or to data that affects the function of a machine. The Examiner argues that the applicants have not shown how the claimed subject matter affects the function of a computer. Accordingly, Claim 69 has been amended to recite that a comparison function, of a computer comprising the computer memory, compares an output signal matrix with the output signal data structure database to deduce characteristics of a stimulus applied to a living thing. Applicants submit that amended Claim 69 more clearly identifies how the claimed subject matter affects the function of a computer, in particular the ability of a computer to make a comparison between an output signal matrix and an output signal data structure database in order to deduce characteristics of a stimulus applied to a living thing. Support for the amendments to Claim 69 is found in the specification at least at page 7, lines 14-18. Applicants submit that amended Claim 69 defines patentable subject matter and is in condition for allowance.

Rejection of Claims 38-53, 55-66, 68-83, and 85 Under 35 U.S.C. § 103(a)

Claims 38-53, 55-66, 68-83, and 85 have been rejected under 35 U.S.C. § 103(a) as being unpatentable over Gress et al., in view of Granelli-Piperno et al., in view of Fodor et al. (U.S. Patent No. 5,800,992). Applicants reiterate the arguments made in response to the same rejection in the amendment filed July 12, 2004. For the sake of brevity, applicants have not repeated all of these arguments in this response, but refer the Examiner to the response filed on July 12, 2004.

In the Office Action mailed August 20, 2004, the Examiner further argues that Gress et al. does not teach away from sequenced array elements. The Examiner states that Gress et al.

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does not sequence all array elements in order to reduce labor involved in sequencing those elements that do not hybridize to probes of interest and are therefore elements that are not of interest.

Applicants submit that Gress et al. did not sequence all the array elements because the use of sequenced array elements is not necessary for the successful use of the Gress et al. invention. Consequently, as described more fully herein, applicants submit that there is no motivation to modify the Gress et al. invention to incorporate sequenced array elements, because the use of sequenced array elements is not necessary for the successful use of the Gress et al. invention, and one of ordinary skill in the art would not be motivated to expend considerable time and money unnecessarily sequencing thousands of array elements.

Gress et al. disclose a method for characterizing large numbers of cDNA library clones that is useful, for example, to identify cDNA clones that are abundantly expressed in several tissues, and that are likely to encode proteins involved in structural and regulatory functions in every cell (see, Gress et al., page 610, first column, lines 17-26). In the practice of the Gress et al. method, thousands of unidentified cDNA clones from human fetal brain, and from *Drosophila* embryos, are arrayed on a nitrocellulose filter, and hybridized against a labeled cDNA pool derived from mouse tissues (see, Gress et al., page 610, "Materials and methods" section). Thus, the method of Gress et al. does not require any knowledge of the identity or sequence of the cDNA clones that are being sought. The method permits screening of numerous (e.g., thousands) of cDNA molecules isolated from a cell type or tissue, to identify the highly expressed clones.

In order to use an array of sequenced cDNA molecules in the practice of the Gress et al. method, the thousands of cDNA molecules that are to be arrayed on a substrate would first have to be sequenced. An array of cDNA-specific oligonucleotide hybridization probes could be used instead of the corresponding cDNAs, but each of the thousands of cDNA molecules would have

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to be sufficiently sequenced to identify an oligonucleotide sequence element that is unique to each cDNA, and that acts as a cDNA-specific hybridization probe under defined hybridization conditions. Sequencing the thousands of cDNAs arrayed on a substrate in the practice of the Gress et al. invention would be very tedious and time-consuming, and, more importantly, is unnecessary. Accordingly, applicants submit that one of ordinary skill in the art would not be motivated to modify the Gress et al. invention to use sequenced array elements instead of unsequenced array elements.

Applicants respectfully request that the rejection of Claims 38-53, 55-66, 68-83, and 85 under 35 U.S.C. § 103(a) be withdrawn.

Rejection of Claims 38, 49-51, 54, 56, 63-65, 67, 70, 80-82, and 84 Under 35 U.S.C. § 103(a)

Claims 38, 49-51, 54, 56, 63-65, 67, 70, 80-82, and 84 have been rejected under 35 U.S.C. § 103(a) as being unpatentable over Gress et al. in view of Granelli-Piperno et al. in view of Fodor et al. as applied to Claims 38-53, 55-66, 68-83, and 85 above, and further in view of Watson et al. The Examiner characterizes the rejected Claims as being drawn to assays utilizing fungal cells, and cites Watson et al., pp. 573-575, for its teaching that these cells contain genes that are regulated by stimuli such as metabolites.

For the reasons set forth in the preceding section, applicants submit that it is not obvious to combine the teachings of Gress et al. and Fodor et al. as suggested by the Examiner. This deficiency is not cured by the teachings of either Granelli-Piperno et al. or Watson et al.

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REMARKS

In view of the foregoing arguments and claim amendment, applicants submit that all of the pending claims are in condition for allowance. Reconsideration and favorable action are requested.

Respectfully submitted,

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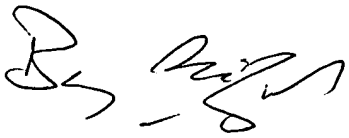

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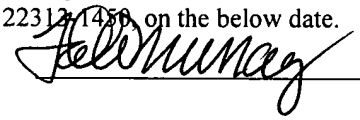
Date: February 4, 2005 

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